

**IN THE SPECIFICATION:**

Please enter the substitute Specification included in the instant filing.

**IN THE CLAIMS:**

Please enter the following amended claims:

1. (Currently amended) A method for identifying a the-candidate protein proteins that may be useful as an anti-infective-infectives, which comprises:
- i) calculating computationally ~~the~~-different sequence--based attributes from all the protein sequences of a the-selected pathogenic organism, organisms.
  - ii) clustering computationally all the protein sequences the proteins-of said selected pathogenic organism a-genome-based on the these-sequence-based attributes of step i) using Principle Component Analysis,-
  - iii) identifying computationally ~~the-outlier protein proteins~~-sequences from the selected pathogenic organism protein sequences which are excluded from a the-main cluster,-
  - iv) matching an the-outlier protein sequence with ~~the~~-protein sequences in various databases,-
  - v) selecting an the-unique outlier protein sequence sequences-not homologous to any of the-protein sequence in said various databases sequences-searched above, and -
  - vi) validating computationally the protein sequence of step v) sequences-as a candidate anti-infective infectives-by comparing said sequence with ~~the~~-known protein sequences of the selected pathogenic organism that are biochemically characterized-in-the pathogen-genome.

2. (Currently amended) TheA method according to ~~elaimed in~~-claim 1, wherein, the selected pathogenic organism is a member selected from the group consisting of *Borrelia burgdorferi*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Leishmania major*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Mycobacterium tuberculosis*, *Neisseria meningitis*, *Pseudomonas aeruginosa*, *Plasmodium falciparum*, *Rickettsia prowazekii*, *Treponema pallidum*, and *Vibrio cholerae*. protein sequence data is taken from any organism, specifically but not limited to organisms such as B.burgdorferi, C.jejuni, C.pneumoniae, C.trachomatis, H.influenzae, H.pylori, L.major, M.genetalium, M.pneumoniae, M.tuberculosis, N.meningitis, P.aeruginosa, P.falciparum, R.prowazekii, T.pallidum, V.cholerae.

3. (Currently amended) TheA method according to ~~elaimed in~~-claim 1, wherein said different sequence-based attributes are one or more of ~~used for identification of candidate anti-infective proteins are~~ selected from the group ~~comprising of a fixed protein attribute, and one or more of a variable protein attribute~~ attributes, or a combination thereof.

4. (Currently amended) TheA method according to ~~elaimed in~~-claim 1, wherein said one or more ~~the~~ fixed protein attribute is ~~attributes are~~ selected from the group consisting ~~comprising of~~ percentage of charged amino acids, percentage hydrophobicity, distance of protein sequence from a fixed reference frame, measure of dipeptide complexity of said candidate protein, and measure of hydrophobic distance from a fixed reference frame.

5. (Currently amended) TheA method according to ~~as elaimed in~~-claim 3, wherein said one or more ~~the~~ variable protein attribute is ~~the~~ distance of said candidate ~~the~~ protein sequence from a variable reference frame.

6. (Currently amended) TheA method according to as claimed in claim 1, wherein the clustering of step ii) cluster analysis is carried out by Principle Analysis Technique using correlation coefficient between the attributes.

7. (Currently amended) TheA method according to as claimed in claim 1, wherein the steps i) to iv) and vi) are performed computationally.

8. (Currently amended) TheA method according to as claimed in claim 1, wherein the clustering of step ii) the proteins is based upon analysis of sequence attributes, and not upon instead of sequence pattern linked to biochemical functions. an unique outlier protein sequence not homologous to any protein sequence in said various databases

9. (Currently amended) The method according to A methos as claimed in claim 1, wherein the unique outlier protein sequence of step v) is a protein of one member selected from the group consisting of sequences non homologous to the known anti infective sequences specifically in the following pathogens but not limited to, such as *Borrelia burgdorferi*, *Campylobacter jejuni*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Leishmania major*, *Mycoplasma genitalium*, *Mycoplasma pneumoniae*, *Mycobacterium tuberculosis*, *Neisseria meningitis*, *Pseudomonas aeruginosa*, *Plasmodium falciparum*, *Rickettsia prowazekii*, *Treponema pallidum*, and *Vibrio cholerae* *B.burgdorferi*, *C.jejuni*, *C.pneumoniae*, *C.trachomatis*, *H.influenzae*, *H.pylori*, *L.major*, *M.genetalium*, *M.pneumoniae*, *M.tuberculosis*, *N.meningitis*, *P.aeruginosa*, *P.falciparum*, *R.prowazekii*, *T.pallidum*, *V.cholerae*.

10. (Currently amended) TheA method according to as claimed in claim 1-, wherein the unique outlier protein is a member selected from the group consisting of the amino acid sequences of

SEQ ID NOs:1-31~~sequences obtained by the method of invention that can serve as potential anti-infective candidates as listed in Table 1 and list 1.~~

11. (Currently amended) TheA method according to as claimed in claim 1-, wherein the The unique outlier protein is a member selected from the group consisting of the amino acid sequences of SEQ ID NOs:32-118~~hypothetical protein sequences from pathogenic genomes that can serve as anti-infective candidates listed in Table 2.~~

12. (Canceled).

13. (Currently amended) TheA method according to as claimed in claim 1-, wherein all of said steps taking place computationally are performed on a the computer system comprising~~comprises:~~

a) \_\_\_\_\_ a central processing unit (CPU) that (1) executes, -executing DISTANCE program, (2) that executes a program that clusters, -clustering of the protein sequences based on different attributes using by Principle Component Analysis, and (3) that stores all results all stored in a memory device accessed by said CPU-,

b) \_\_\_\_\_ a display on which the CPU central processing unit displays all results the screens of the above mentioned said programs in response to user inputs; and

c) \_\_\_\_\_ a user interface device.

14. (Currently amended) TheA method according to as claimed in claim 1-, wherein the candidate unique outlier hypothetical protein may sequences from pathogenic genomes that can be used for a diagnostic purpose.

15. (Currently amended) TheA method according to as claimed in claim 1-, wherein the candidate unique outlier hypothetical protein may sequences from pathogenic genomes that can be used as a vaccine candidate~~candidates.~~

16. (Currently amended) TheA method according to ~~as claimed in claim 1-~~, wherein  
the candidate ~~The unique outlier hypothetical protein~~ may ~~sequences from pathogenic genomes~~  
~~that can be used for a therapeutic purpose~~purposes.

17-19. (canceled).

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